

Fig. S1

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PA4352      ---MKRILVATDLSRSELAVMRAAALAKARNAELTVLNVLDDDDQPPVLIAPQRLAIANL 57
PA5027      --MIRHLLVAHDLTPEADVALARAAQLARQHDARVSLHVVYD----PGLSASAVKTVSAM 54
PA4328      -MNLHNLLVVVDPSSDEQPALTRAQWIAEHS GASVELLLCDFN---PALDGGFFDSSHSL 56
PA1789      MQAIRSILVVEPDQLEGLALKRAQLIAGVTQSHLHLLVCEKR-----RDHSAAL 50
           :: :*. :      * : ** : *      : : : *      :

PA4352      LEVNGQALKERL-----GVESKAIVRVGDVV-VINAVAEIIGADLLVMGAH 103
PA5027      LQLK--RKEAGL-----DEDSAIHLFRGQPID-GILQQTRALEPDLLLMGAH 98
PA4328      QRARDLYLDERVTWLEQLSMPLQQAGIRTQVEAQWGKPLDRMVLQRVGETRPDLVLKSTR 116
PA1789      NDLAQELREE-----GYSVSTNQAWKDSLHQTI IAEQQAECCGLI IKQHF 95
           .           .           ..: :           .*: :

PA4352      RHTPLRDLFIGTTLERVVRNAKIPVLRAGAPE--EEYRRVLLALDFS----PTSTRAVQ 157
PA5027      -HQKTFERFGNTTLDQVRRSRVPVLLAVREAD--EPYRQALSALDFS----QCACTALR 151
PA4328      KHNLRLRLLGNSDWQLIRHCPQLWLHVHDAWRGQRLCAALDPLHASDKPAALDHRLIA 176
PA1789      PDNPLKKAILTDPDDWKLRFAPCPVLMTKTARP--WTGGKILAAVDVGNNDGEHRSLHAG 153
           .           :           :*: .      * : .           * ..: .

PA4352      MAGQLGFLDAASLTALHAFEPFAKMMRYSGIKEDRVEHYVDQEELKANVELRDYVAGLG 217
PA5027      QAYRLLPVEAD-LHALHVFESPDGVL---GLPRQNAHLATQAGLIEQLLSDEQERLPG 207
PA4328      AARQLEASLGLRADYLHTHAAMPSSLFFDAEMLAGYERFVLQHEERHRQAFD DLLAAYPE 236
PA1789      IISHAYDIAGLAKATLHVISAHPMSLS----SADPTFQLSETIEARYREACRTFQAEYG 209
           :           .           **. .           : :           .

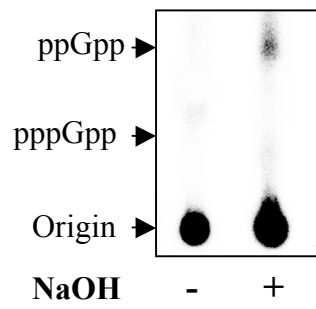
PA4352      LGREDIQLRVGEGLPINVIMTEVRRQAPQLTVLGTQGLTGFRRALIGSVAEAAALGDLPCD 277
PA5027      VG-PQLSHEVVPGLVPYSLDAALKQRQPELLALGRHSRNALMQALLGNLAQRYLRQPSCD 266
PA4328      IA--AERRHLLAGYAEQAIPDFVRANDIDL LLMGAVARGHLDNALIGQTAERVLEEVCD 294
PA1789      FS--DEQLHIEEGPADVLI PRTAQKLDVAVTVIGTVARTGLSGALIGNTAEVVLDTLES D 267
           ..           .: *           :           :           : : * .           : **:* . * : *           . *

PA4352      VLAVPPKRD----- 286
PA5027      VLVTS----- 271
PA4328      LLVLKPTNDI----- 304
PA1789      VLVLPKDDIIAHLEELASKE 287
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**Fig. S1: Alignment of all four universal stress proteins of *P. aeruginosa***

Alignment was performed with amino acid sequences of PA4352, PA5027, PA4328 and PA1789 using the ClustelW2 tool of the EBI database ([www.ebi.ac.uk](http://www.ebi.ac.uk)). “\*” marks identical amino acids in all sequences, “:” marks conserved amino acid substitution and “.” marks semi-conserved amino acid substitutions. PA4352 shares an identity of 30.6 % with PA5027, 25.8 % with PA1789 and 23.0 % with PA4328.

Fig. S2:



**Fig. S2: Accumulation of ppGpp in response to alkaline pH in defined minimal medium.**

Wild type was grown to exponential phase in MOPS minimal medium, was prelabelled for 15 h with  $^{32}\text{P}_i$  and was subsequently treated with 20 mM NaOH to achieve pH values of 8.5 for additional 15 minutes (lane +). Control culture was left untreated (lane -).

MOPS minimal medium:

40 mM MOPS	0.1 mM $\text{CaCl}_2$
20 mM KOH	1 mM $\text{MgCl}_2$
20 mM $\text{NH}_4\text{Cl}$	30 mM Succinate
100 mM NaCl	Trace metals
1 mM $\text{KH}_2\text{PO}_4$	